

CLAIMS

1 1. A process for altering the host range of
2 Bacillus toxins which comprises recombining in vitro
3 the variable region of two or more Bacillus toxin genes.

1 2. A process, according to claim 1, wherein the
2 Bacillus is a Bacillus thuringiensis.

1 3. A process, according to claim 2, wherein
2 variable regions of Bacillus thuringiensis var.
3 kurstaki HD-1 and Bacillus thuringiensis var.
4 kurstaki HD-73 are recombined in vitro to give genes
5 encoding chimeric toxins having altered host ranges.

1 4. DNA, denoted pEW3, encoding a chimeric toxin
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400
4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
5 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
6 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
7 GATTTGTGTT AGSACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
8 CAATGGGACG CATTCTTGTT ACAAATTGAA CAGTTAATTA ACCAAGAAT
9 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
11 ACTAATCCAG CATTAGGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
12 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
13 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
14 TTGAGAGATG TTTAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
19 ATCCAATTCTG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
20 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAATA
ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
TGGAACATAT GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA

21 CCTAGGCAAG GATTTAGTCA TCGATTAAAGC CATGTTTCAA TGTTTCGTTC 1700
 22 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 (start HD-1) CCAACGT TTTCTTGGCA GCATCGGAGT 1900
 23 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 24 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 GATTACAGG ASSAGATATT CTTCAAGAA CTTACCTGG CCAGATTTC
 25 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 26 GAAGACCTAT TAATCAGGGT AATTTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 27 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 28 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTC GGCAGAAGTA
 29 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 30 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 31 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 32 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 33 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 34 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 35 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 TGTGCCAGGT ACGGGTTCC TATGSCCGCT TTCAGCCCAA AGTCCAATCG 2900
 36 GAAAGTGTGG AGAGCCGAAT CGATGCGGCG CACACCTTGA ATGGAATCCT
 37 GACTTAGATT GTTCGTGTAG GGATGAGAA AAGTGTGCCC ATCATTCGCA 3000
 TCATTTCTCC TTAGACATTG ATGTAGSATG TACAGACTTA AATGAGGACC
 38 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 39 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAGGCGCT
 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAT 3200
 40 TGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 41 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 TGCCATGATT CATGCGGCG AGTAAACGTGT TCATAGCATT CGAGAAGCTT
 42 ATCTGCCTGA GCTGTCTGTG ATTCGCGGTG TCAATGCGGC TATTTTGA 3400
 GAATTAGAAG GGCSTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 43 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGAACGTGA 3500
 44 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 45 CTTCCGGAAT GGGAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 46 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 47 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 TGATTACT GTAAATCAAG AAGAATACGG AAGTGCCTAC ACTTCTCGTA 3800
 48 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGCCTCAGTC
 TATGAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 49 TAACAGAGGG TATAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 50 AAGAAATAGA ATACTTCCCA GAAACCGATA AAGTATGGAT TGAGATTGGA 4000
 51 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54
55 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
56 T G Y T F I D I S L S L T Q F L L S E F V P G A G F V L G L
57 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
58 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
59 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
60 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
61 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
62 Y N T G L E R V W G F D S R D W V R Y N Q F R R E L T L T V
63 L D I V A L F F N Y D S R R Y P I R T V S Q L T R E I Y T N
64 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
65 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
66 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
67 T L S S T L Y R R F F N I G I N N Q Q L S V L D G T E F A Y
68 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V
69 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
70 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
71 N L G S G T S V V K G P G E T G G D I L R R T S P G Q I S T
72 L R V N I T A F L S Q R Y A V R I R Y A S T T N L Q F H T S
73 I D G R F I N Q G N F S A T M S S G S N L Q S G S F R T V G
74 F T T F F N F S N G S S V F T L S A H V F N S G N E V Y I D
75 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
76 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
77 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
78 G I N R Q E L D R G W R G S T D I T I Q G G D D V F K E N Y V
79 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
80 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
81 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
A A D K R V H S I R E A Y L F E L S V I P G V N A A I F E E
L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
E L L L M E E.

10035050 122704

5. DNA, denoted pEW4, encoding a chimeric toxin,
having pesticidal activity, as follows:

(start HD-1) ATGG ATAACAATCC GAACATCAAT
1 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
2 TGGAGAAAGA ATAGAACTG GTTACACCCC AATCGATATT TCCTTGCTCC
3 TAACGCAATT TCTTTTGAGT GAATTTGTTT CCGGTGCTGG ATTTGTGTTA 700
4 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
5 ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
6 CTAGGAACCA AGCCATTCTT AGATTAGAAG GACTAAGCAA TCTTTATCAA
7 ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
8 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
9 CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
10 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
11 TTCAGTGTTT GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
12 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
13 CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
14 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
15 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCTGA 1300
16 ACASTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
17 TTTTGATGGT AGTTTTCTGT GAATGCTCA GAGAATAGAA CAGAATATTA 1400
18 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
19 GTGCATAGAG GCTTTAATTA TTGCTCAGGG CATCAAATAA CAGCTTCTCC 1500
20 TGTAGGGTTT TCAGGACCAG AATTCGCAAT CCCTTTATTT GGGAAATGCGG
21 GGAATGCAGC TCCACCCGTA CTGCTCAT TAAGTGGTTT GGGGATTTT 1600
22 AGAACATTAT CTTACCTTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
23 AAATAATCAG GAACTGTTTG TCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
24 CCCTAACGAC CAACTTGCCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
25 GATTCACTAG ATGTAAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
26 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
27 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
(start HD-73) CCT ATGTTCTCTT
28 GGATACATCG TAGTGTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
29 ACTCAATCC CTGCACTGAA GGGAACTTT CTTTTTAATG GTTCTGTAAT
30 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
31 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
32 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
33 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTT TCCAATACAG
34 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
35 TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
36 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
37 TTATTCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
38 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
39 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
40 ATTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
41 GTCAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
42 AAATTTCAA GACATTAATA GGCAACCAGA ACGTGGGTGG GCGGGAAGTA 2500
43 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGA AAATTACGTC
44 AACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
45 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
46 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
47 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTAT GGCCGCTTTC

36 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 38 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGSATGTAC 2900
 39 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 40 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 41 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 42 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 43 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 44 CAAGCGGATA CGAATATTGC CATGATTTCAT GCGGCAGATA AACGTGTTCA 3200
 45 TAGCATTCTGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 46 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 47 CTATATGATG CGAGAAATGT CATTAAATAT GGTGATTTTA ATAATGGCTT
 48 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 49 AACGTTCTGG CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 50 GTTCGTGTCT GTCCGGGTCT TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 51 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 52 CAGACGAACT GAAGTTTAGC AACTGCTAG AAGAGGAAAT CTATCCAAAT 3600
 53 AACACGGTAA CGTGTAAATGA TTATCTGTA AATCAAGAAG AATACGGAGG
 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 TATGGATTGA GATTGGAGAA ACBGAAGGAA CATTATCGT GGACAGCGTG 3900
 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
 55 T G Y T F I D I S L S L T Q F L L S E F V P G A G F V L G L
 56 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
 57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 62 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 63 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 64 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 65 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T
 66 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
 67 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
 68 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
 69 R P M F S W I H R S A E F N N I I A S D S I T Q I F A V K G
 70 N F L F N G S V I S G P G F T G S D L V R L N S S G N N I Q
 71 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
 72 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
 73 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
 74 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
 75 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
 76 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
 77 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
 78 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
 79 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
 80 G T G S L W P L S A Q S P I G K C G E F N R C A P H L E W N
 F D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
 K F L V G E A L A R V K R A E K K W R D K R E K L E W E T N
 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
 C W N V R G H V D V E E Q N N Q R S V L V V P E W E A E V S
 Q E V R V C F G R G Y I L R V T A Y K E G Y G E G C V T I H
 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
 S V E L L L M E E .

- 1 6. DNA, denoted pACB-1, encoding a chimeric toxin,
 2 having pesticidal activity, as follows:

		(start	HD-73)	ATG	GATAACAATC	400
3	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA	
4	GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT	500
5	TTCTTTGTCG	CTAACGCAAT	TTCTTTTGAG	TGAATTTGTT	CCCGGTGCTG	
6	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATTTT	TGGTCCCTCT	600
7	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAGTTAATTA	ACCAAGAAT	
8	AGAAGAATTC	GCTAGGAACC	AAGCCATTTT	TAGATTAGAA	GGACTAAGCA	700
9	ATCTTTATCA	AATTTACGCA	GAATCTTTTA	GAGAGTGGGA	AGCAGATCCT	
10	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCATTTC	ATGACATGAA	800
11	CAGTGGCCTT	ACAACCGCTA	TTCTCTTTT	TGCAGTTCAA	AATTATCAAG	
12	TTCTCTTTT	ATCAGTATAT	GTTCAAGCTG	CAAATTTACA	TTTATCAGTT	900
13	TTGAGAGATG	TTTCAGTGTT	TGGACAAAGG	TGGGGATTG	ATGCCGCGAC	
14	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG	1000
15	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
16	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
17	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
18	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
19	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
20	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
21	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
22	ATGGCTTCTC	CTGTAGGGTT	TTGGGGCCA	GAATTCACTT	TTCCGCTATA	1400
23	TGGAACATATG	GGAAATGCAG	CTCGACAAGA	ACGTATTGTT	GCTCAACTAG	
24	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
25	AATATAGGGA	TAAATAATCA	ACCACTATCT	GTTCTTGACG	GGACAGAATT	
26	TGCTTATGGA	ACCTCCTCAA	ATTGCCCATC	CGCTGTATAC	AGAAAAAGCG	1600
27	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
28	CCTAGGCAAG	AATTTAGTCA	TGGATTAAAGC	CATGTTTCAA	TGTTTCGTTC	1700
29	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
30	(start	HD-1)	CCAACGT	TTTCTTGGCA	GCATCGCAGT	1900
31	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
32	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTGCTT	AAAGGACCAG	2000
33	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
34	ACCTTAAGAG	TAAATATTAC	TGCACCATT	TCACAAAGAT	ATCGGGTAG	2100
35	AATTGCTAC	GCTTCTACTA	CAAAATTTACA	ATTCCATACA	TCAATTGACG	
36	GAAGACCTAT	TAATCAGGGT	AATTTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
37	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
38	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
39	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
40	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
41	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
42	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
43	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
44	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
45	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
46	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
47	TGATGAGTGC	TATCCAACTG	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
48	TAAAGAGCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
49	GACTTAGAAA	TCTATTTAAT	TGCTACCAAT	GCAAAACATG	AAACAGTAAA	
50	TGTGCCAGGT	ACGGGTTTCT	TATGGCCGCT	TTCAGCCCAA	AGTCCAATCG	2900
51	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
52	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTGCGA	3000
53	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
54						

55 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAGAAT 3200
 58 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGTAA 3400
 62 GAATTAGAAG GGCSTATTTT CACTGCATTC TCCCTATATG ATGCBAGAAA
 63 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 65 CTTCCGGAAT GGGGAAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGAGAAAG
 67 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CTTTCCGTAC CAGGTGATTA TCGTCAAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
 77 ACB-1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 82 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
 83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 86 L D I V A L F F N Y D S R R Y F I R T V S Q L T R E I Y T N
 87 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 88 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 91 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 92 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 93 P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T
 94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G


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97  F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
98  R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99  S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K M G D F N N G L S C W
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E .

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7. DNA, denoted p^{SW1}, encoding a chimeric toxin, having pesticidal activity, as follows:

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3          (start HD-73)          ATG GATAACAATC 400
4  CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
5  GAAGTATTAG GTGGAGAAAG AATGAAACT GGTACACCC CAATCGATAT 500
6  TTCCTTGTCT CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGTCTG
7  GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
8  CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
9  AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700
10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
11 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
12 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
13 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
14 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGSC AACTATACAG 1000
16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
17 GATTGTAGAG ATTGGGTAAG GTATAATCAA JTTAGAAGAG AATTAACACT 1100
18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
19 ATCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
20 GTATTAGAAA ATTTTGATGG TAGTTTTTCA GGTCTCGGCTC AGGGCATAGA
21 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
22 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAATA
23 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
24 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
25 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
26 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT

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27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 28 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 29 CCTAGGCAAG GATTTAGTCA TCGATTAGC CATGTTTCAA TGTTTCGTC 1700
 30 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 32 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 33 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 34 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTC
 35 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 36 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 37 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 39 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAASTA
 41 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCAGAAAAGG CGGTGAATGA 2400
 42 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 43 ATCATATTGA TCAAGSTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 44 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAC ATGCGAAGCG
 45 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 46 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 47 GGAGGCGATG ACGTATTCAA AGAGAAATAC GTTACGCTAT TGGGTACCTT 2700
 48 TGATAGTGTC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 49 TAAAGGCCTA TACCCGTTAT CAATTAGAG GGTATATCGA AGATAGTCAA 2800
 50 GACTTAGAAA TCTATTTAAT TCGATACAAT GCAAAACATG AAACAGTAAA
 51 TGTGCCAGGT ACGGGTTTCT TATGSCCGCT TTCAGCCCAA AGTCCAATCG 2900
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 55 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGA AAAAT 3200
 58 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGSCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 62 GAATTAGAAG GCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 63 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGSCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 65 CTTCCGGAAT GGGGAAGCAGA AGTGTCACAA GAAGTTCTGT TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 67 GTTGCGTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TCGCTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
77 SYW1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
79 T G Y T P I D I S L S L T Q F L L S E F V F G A G F V L G L
80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
87 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
88 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
91 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
92 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
94 N L G S G T S V V K G P G F T G S D I L R R T S P G G Q I S T
95 L R V N I T A P L S Q R Y R Y R I R Y A S T T N L Q F H T S
96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E N K Q E L S E K V G H A K R I T S D E R N L L Q D P N F R
101 G I N R Q L D R G W R K S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E .

8. A chimeric toxin, EW3, having pesticidal activity, having the following amino acid sequence:

MDNNPNINECIPYNCLSNPEVEVLGGSERIE
 TGYTFIDISLSLTQFLLEFVPGAGFVVLGL
 VDIIWGIFGPGSQWDAFLVQIEQLINQRIEE
 FARNQAISRLEGLSNLYQIYAESFREWEADV
 PTNPAALREEMRIQFNDMMNSALTTAIFLFAV
 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 RWGFDAATINSRYNDLTRLIGNYT DYAVRW
 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
 LDIVALFFPNYDSRRYPPIRTVSSQLTREIYTN
 FVLENFDGSGFRGSAQGGIERSIRSPHLM DIL
 NSITIIYTDAHRGYYYSWGHQIMASPVGFGSG
 PEFTTFPLYGTMGNAAPQQQRIVAQLGGGVYR
 TSSSTLYRRPFFNIGINNQQQLSVLDGTEFAY
 GTSSSNLPSAVYRKSGTVDLSLDEIPFQNNNV
 PPRQGFSHRLSHVSMFSSGFSNSSVSIIRA
 PTFSWQHRSAEFNNIIPSSQITQIPLTKST
 NLGSGTSSVVKGPBFTGGDILRRTSPGQIST
 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
 IDGRFINQGNFSATMTSSSSNLQSGSFRTVG
 FTTFFNFSSNGSSVETLSAHVFNSGNEVYID
 RIEFVFAEVTFEAEYDLERAQKAVNELFTS
 SNQIGLKTDTVTDYHIDQVSNLVECLSDFC
 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 GINROLDRGWGSGSTDITIQGGDDVFKENYV
 TLLGTFDECYFTYLYQKIDESKLLKAYTRYQ
 LRGYIEDSQDLEIYLYIRYNKHEHVNVFGT
 GSLWPLSAQSPIGKCGEPNRCAPHLEWNFD
 LDCSCRDGEEKCAHSHHFSLDIDVGCOTDLN
 EDLGVWVIFKIKTDGHDHARLGNLEFLEEKFP
 LVGEALARVKRAEKKWRDKREKLEWETNIV
 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 AADKRVHSIREAYLPFLSVIPGVNAAIFEE
 LEGRIFTAFSLYDARNVINKNGDFNNGLSCW
 NVKGHV DVEEQNNQORSVLVLPEWEAEVSGE
 VRVCFGRGYILRVTA YKEGYGEGCVTIHEI
 ENNTDELKFSNCEVEEIEYPNNTVTCNDYTV
 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
 EEKSYTDGRRENFCFNRGYRDTPLFPVGY
 VTKELYFPETDKVWIEIGETEGT FIVDSV
 ELLLMEE

and mutants thereof which do not alter the protein secondary structure.

9. A chimeric toxin, EW4, having pesticidal activity, having the following amino acid sequence:

MDNNPNIN ECIPYNC LSNPEVEVLGG ERIE
 TGYTPIDISLSLTQFL LSEFVPGAGFVLGL
 VDIIWGIFGFSQWDAFPVQIEQLINQRIEE
 FARNQAI SRLEGLSNLYQIYAESFREWEAD
 PTNPALREEMRIQFNDMNSALT TAIPLLAV
 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ
 RWGFDAATINSRYNDLTR LIGNYT DYAVRW
 YNTGLERVWGPDSRDWVRYNQFRRELT LT V
 LDIVALFSNYDSRRYP IRTVSQLTREIYTN
 FVLENFDGSGFRGMAQR IEQNI RQPHLM DIL
 NSIT IYT DVH RGFNYWSGHQITASPVGFSG
 PEFAPFLFGNAGNAAPPV LVSLTGLGIFRT
 LSSPLYRRIILGSGFPNNQELFVLDGTEFSF
 ASLTTNLPSTIYFQRGTVDSDL DVIPPQD NS
 VFPFRAGF SHRLSHVTMLSQAAGAVYTLRAQ
 RPFMF SWIHRSAEFNNIIASDSITQIPAVKG
 NFLFNGSVISGFGGTGGDLVRLNSSSGNNIQ
 NRGYIEVPIHF PSTSTRYRVRYASVTPI
 HLN VN WGNSSIFSNTVPATATSLDNLQSSD
 FGYFESANAF TSSLGNI VGV RNFSGTAGVI
 IDRFEFIPVTATLEAEYNLERAKAVNALF
 TSTNQ LGLKTNTD YHIDQVSNLV TYLSDE
 FCLDEKRELSEKVKHAKRLSDERNLLQDSN
 FKDINRQPERG WGGSTGITIQGGDDVFKEN
 YVTL SGT FDECYFTYLYQK IDESKLKAFT R
 YQLRGYIEDSQDLEIYLIRYN AKHETVNV P
 GTGSLWFLSAQSPIGKCGEPNRCAPHLEWN
 PDLDCSCR DGEKCAHHS HHFSLDIDVGCTD
 LNE DLGVWVIFKIKTQDGHARLG NLEFLEE
 KP LVGEALARVKRAEKKWRDKREKLEWETN
 IVYKEAKESVDALFVNSQYDQLQADTNIAM
 IHAADKRVHSIREAYLP ELSVIPGVNAAIF
 EEL EGRIFTAFSLYDARNV IKN GDFNGLS
 CWNVKGHVDVEEQNNQR SVLVVPEWEAEVS
 QEV RVCPGRGYILRV TAYKEGYGEGCVTIH
 EIENN TDELKFSNCVEE EIYPNNTVTCNDY
 TVNQEEYGGAYTSRNRGYNEAPSVPADYAS
 VYEEKSYTDGRRENPC EFNRGYRDYTPLPV
 GYVTKELEYFPETDKVWIEIGETEGTFIVD
 SVELLLMEE

and muteins thereof which do not alter the protein secondary structure.

-58-

10. A chimeric toxin, ACB-1, having pesticidal activity, having the following amino acid sequence:

MDMNPNI NECI PYNCLSNPEVEVLGGERRIE
 TGYTPIDISLSLTQFLLSEFVFGAGFYLGGL
 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
 FARNQAISRLEGLSNLYQIYAESFREWEAD
 PTNPALREEMRIQFNDMNSALTTTAIPLFAV
 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 RWGFDAAATINSRYNDLTRLIGNYTDDYAVRW
 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
 LDIVALFPNYDSRRYPPIRTVSQLTREIYTN
 PVLENFDGSGFRGSAQGGIERSIRSPHLMDFIL
 NSITIIYTDAHRGYYYSWGHQIMASPVGGVYR
 PEFTTFPLYGTMGNAAPQQRIVAQLDGTGFAY
 TSSSTLYRRPFNIGINNQQLSVLDTGFAY
 GTSSSNLPSAVYRKSGTVDSLNEIPPQNNNV
 PPRQEFSSHRLSHVSMFRSGFSNSSVSIRA
 PTFSWQHRSAAEFNNIIFSSQITQIPLTKST
 NLGSGTSSVVKGPFFTGGDILRRTSPGQIST
 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
 IDGRPINQGNFSATMSSSGSNLQSGSFRTVG
 FTTPFNFNSNGSSVFTLSAHVFNSGNEVYID
 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 SNQIGLKTDTVTDYHIDQVSNLVECLSDFC
 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 GINRQLDRGWGSGTDITIQGGDDVFKENYV
 TLLGTFDECYPTYLYQKIDESKCLKAYTRYQ
 LRGYIEDSQDLEIYLYIRYNKHETVNVPGT
 GSWLWFLSAQSPIGKCGEFPNRCAPHLEWNP
 LDSCSCRDGEEKCAHHSHHFSLDIDVGCDDL
 EDLGVWVIFKIKTQDGHARLGNLEFLEEK
 LVGEALARVKRAEKKWRDKREKLEWETNIV
 YKEAKESVDALFVNSQYDQLQADTNIAH
 AADKRVHSIREAYLPPELSVIPGVNAAFEE
 LEGRIFTAFSLYDARNVIKNGDFNGLSCW
 NVKGHVVDVEEQNNQRSVLVLPEWEAEVSE
 VRVCPGGRGYILRVTAAYKEGYGEGCVTH
 ENNTDELKFSNCVEEIEYPNNTVTNDYTV
 NQEEYGGAYTSRNRGGYNEAPSVADYASVY
 EEKSYTDGRRNPFCEFNRGYRDYTPLPVGY
 VTKELEYFPETDKVWIEIGETEGTFIVDSV
 ELLLME

and muteins thereof which do not alter the protein secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNIN ECIPYNC LSNPEVEVLGG ERIE
4 TGYTPIDISLSLTQFL LSEFVPGAG FVLGL
5 VDI IWGIFG P SQWDAFLVQ IEQLINQRIEE
6 FARNQAISRLEGLSNLYQ IYAESFREWEAD
7 PTNPALREEMRIQFNDMNSALT TAIPLFAV
8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
9 RWGFD AATINSRYNDLT RLIGNYTDYAVRW
10 YNTGLERVWGPDSRDWVRYNQFRRELT LT V
11 LDIV ALFPNYDSRRYP IRTVSQLTREIYTN
12 PVLENFDGSGFRGSAQG IEGSIRSPHLM DIL
13 NSIT IYTD AHKG EY YWSGHQ IMA SPVGFSG
14 PEF TFP LYGT MGN AAPQQRI VAQLGQG VYR
15 T LSSSTLYRRPFNIGINNQQQLSVLDGTEFAY
16 GTSSSNLP S AVYRKSGTVD SLDEIPPQNNNV
17 PPRQG GFSHRLSHVSMFRSGFSNS SVSIRRA
18 PTFSWQHRS AEFNNIIPSSQITQIPLTKST
19 NLGSGT SVVKGP GFTGGDILRR TSPGQIST
20 LRVRNITAPLSQR YRVRIRYASTTNLQFHTS
21 IDG RPI NQNGFSATMSSG SNLQSGSFRTVG
22 FTT P FNF SNGSSVFTLSAHVFNSGNEVYID
23 RIEFVPAEVTFEAEYDLE RAQKAVNELFTS
24 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
26 GINRQLDRGW RGS TDITIQGGDDVFKENYV
27 TLLGT FDECYPT YLYQK IDESKLKAYTRYQ
28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
29 GSLWFLSAQSP I GKC GEPNRCAPHLEWNP D
30 LDCSCR DGEKCAHHSHHFSLDIDV GCTDLN
31 EDLG V W VIFKIKTQDGHARLG NLEFLEEK P
32 LVGEALARVKRAEKKWRDKREKLEWETNI V
33 YKEAKESVDALFVNSQYIDQLQADTNIA MIH
34 AADKR VHSI REAYLP ELSV I P G VN A A I FEE
35 LEGRI FTAFSLYDARNV I KNGDFNNGLS CW
36 NVKGHV DVEEQNNQR SVLVLP EW EAEVSQE
37 VRVCPGRGYILRV TAYKEGYGEGCV TIHEI
38 ENNTDELKFSNCVEEEIYPNNTVT CNDYTV
39 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
40 EEKSYTDGRRENPC EFNRGYRDYTPLPVGY
41 VTKELEYFPETDKVWIEIGETEGTFIVDSV
42 ELLLMEE

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 12. A pesticidal composition comprising pesti-
2 cide-containing substantially intact cells having
3 prolonged pesticidal activity when applied to the
4 environment of a target pest, wherein said pesticide,
5 is a chimeric toxin, is intracellular and is produced
6 as a result of expression of a heterologous gene
7 encoding said chimeric toxin in said cell.

1 13. A pesticidal composition according to claim 12,
2 wherein said cells are killed under protease deacti-
3 vating or cell wall strengthening conditions, while
4 retaining pesticidal activity.

1 14. A pesticidal composition, according to claim 12,
2 wherein said cells are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 15. A pesticidal composition, according to claim 14,
2 wherein said prokaryote is a Bacillus specie selected
3 from a pesticide-producing strain of Bacillus thurin-
4 giensis, consisting of B. thuringiensis M-7, B. thurin-
5 giensis var. kurstaki, B. thuringiensis var. finitimus,
6 B. thuringiensis var. alesti, B. thuringiensis var.
7 sotto, B. thuringiensis var. dendrolimus, B. thurin-
8 giensis var. kenyae, B. thuringiensis var. galleriae,
9 B. thuringiensis var. canadensis, B. thuringiensis var.
10 entomocidus, B. thuringiensis var. subtoxicus, B.
11 thuringiensis var. aizawai, B. thuringiensis var. morri-
12 soni, B. thuringiensis var. ostrinae, B. thuringiensis
13 var. tolworthi, B. thuringiensis var. darmstadiensis,

14 B. thuringiensis var. toumanoffi, B. thuringiensis var.
15 kyushuensis, B. thuringiensis var. thompsoni, B.
16 thuringiensis var. pakistani, B. thuringiensis var.
17 israelensis, B. thuringiensis var. indiana, B. thurin-
18 giensis var. dakota, B. thuringiensis var. tohokuensis,
19 B. thuringiensis var. kumanotoensis, B. thuringiensis
20 var. tochigiensis, B. thuringiensis var. colmeri,
21 B. thuringiensis var. wuhanensis, B. thuringiensis
22 var. tenebrionis, B. thuringiensis var. thuringiensis,
23 and other Bacillus species selected from B. cereus, B.
24 moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1 16. A method of protecting plants against pests
2 which comprises applying to said plants an effective
3 amount of a pesticidal composition comprising pesti-
4 cide-containing substantially intact unicellular
5 microorganisms, wherein said pesticide is a chimeric
6 toxin, is intracellular, and is produced as a result
7 of expression of a heterologous gene encoding said
8 chimeric toxin in said microorganism, and said micro-
9 organism is treated under conditions which prolong
10 the pesticidal activity when said composition is applied
11 to the environment of a target pest.

1 17. A method according to claim 16, wherein said
2 microorganisms are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes, selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 18. A method according to claim 16, wherein said
2 unicellular microorganisms are killed under protease
3 deactivating or cell wall strengthening conditions,
4 while retaining pesticidal activity.

1 19. Substantially intact unicellular microorganism
2 cells containing an intracellular chimeric toxin, which
3 toxin is a result of expression of a heterologous
4 gene encoding said chimeric toxin, wherein said cells
5 are killed under protease deactivating or cell wall
6 strengthening conditions, while retaining pesticidal
7 activity when said cell is applied to the environment
8 of a target pest.

1 20. Cells according to claim 19, wherein said
2 microorganism is a Pseudomonad and said toxin is
3 derived from a B. thuringiensis.

1 21. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW3, encoding a
3 chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400
5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
6 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
7 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
8 GATTTGTGTT AGSACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
9 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
10 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
12 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
13 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
14 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA

16 AGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 17 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCTT TTCCGCTATA 1400
 19 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 20 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 24 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTT 1700
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end HD-73)
 26 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 27 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 28 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCTT AAAGGACCAG 2000
 29 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTACCTGG CCAGATTTCA
 30 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 31 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 32 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 33 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTTAA
 34 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTTCC GGCAGAAGTA
 36 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAGG CGGTGAATGA 2400
 37 GCTGTTTACT TCTTCCAATC AATCGGGTT AAAACAGAT GTGACGGATT
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 39 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 40 ACTTAGTGAT GAGCGGAATT TACTTCAGA TCCAACTTC AGAGGGATCA 2600
 41 ATAGACAATC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 42 GGAGGCGATG ACGTATTCAA AGAGAAATAC GTTACGCTAT TGGGTACCTT 2700
 43 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT AGATCGAAAT
 44 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 46 TGTGCCAGGT ACGGGTTTCT TATGCGCGCT TTCAGCCCAA AGTCCAATCG 2900
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTCGCA 3000
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 51 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 53 TGGAAATGGG AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 54 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 55 TGCCATGATT CATGCGGCGG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 57 GAATTAGAAG GCGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 58 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 59 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 60 CTCCGGAAT GGGAGGAGCA AGTGTCAACA GAAGTTCGTG TCTGTCCGGG 3600
 61 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 62 GTTGGTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 63 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 65 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGCCTCAGTC
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 67 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 68 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 69 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54 MDNNPNINECIPYNCLSNPEVEVLGGGERIE
55 TGYTFIDISLSLTQFLLSEFVPGAGFVLGL
56 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
57 FARNQAISRLEGLSNLYQIYAESFREWEAD
58 PTNPALREEMRIQFNDMNSALTTAIPLFAV
59 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
60 RWGFDAAATINSRDNLDTRLIGNYT DYAVRW
61 YNTGLERVWGPDSRDWVRYNQFRRELTTLTV
62 LDIVALFFPNYDSRRYPIRTVSQLTREIYTN
63 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL
64 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG
65 PEFTFFPLYGTMGNAAPQQRIVAGLGQGVYR
66 TSSSTLYRRFPFNIGINNQQLSVLDGTEFAY
67 GTSSNLP S AVYRKSGTVDSLDEIPPNNNV
68 PPRQGFSHRLSHVSMFRSGFSNSSVSIRA
69 PTFSSWQHRSAEFNNIIFSSQITQIPLTKST
70 NLGSGTSSVVKGGPGETGGDILRRTSPGQIST
71 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
72 IDGRFINQGNFSATMSGSGSNLQSGSFRTVG
73 FTTFPNFSNGSSSVFTLSAHVFNSGNEVYID
74 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
75 SNQIGLKTDTVTDYHIDQVSNLVECLSD EFC
76 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
77 GINRQLDRGW RGSTDITIQGGDDVFKENYV
78 TLLGTDFDECYPTYLYQKIDESK LKAYTRYQ
79 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
80 GSLWFLSAQSPIGKCGEPNRCAPHLEWNP D
LDCSCRDGEKCAHHS HHFSLDIDVGC TDLN
EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P
LVGEALARVKRAEKKWRDKREKLEWETNIV
YKEAKESVDALFVNSQYDQLQADTNIAMIH
AADKRVHSIREAYLP ELSVIPGVNA AIFEE
LEGRIFTA FSLYDARNV I K N G D F N N G L S C W
NVKGHV D V E E Q N N Q R S V L V L P E W E A E V S Q E
VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
ENNTDELKFSNCVEEEEIYPNNTVTCNDYTV
NQEEYGGAYTSRNRGYN EAPSVPADYASVY
EEKSYTDGRRENPC EFN RGYR DY T P L P V G Y
VTKELEYFPETDKVWIEIGETEGTFIVDSV
ELLLMEE.

1 22. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW4, encoding a
3 chimeric toxin, is as follows:

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4           (start HD-1)                   ATGG ATAACAATCC GAACATCAAT
5       GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
6       TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
7       TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
8       GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
9       ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
10       CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
11       ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
12       ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
13       CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
14       TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
15       TTCAGTGTTT GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
16       GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
17       CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
18       TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
19       ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGSTA TCCAATTCGA 1300
20       ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
21       TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
22       GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
23       GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
24       TGTAGSGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGAAATGCGG
25       GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
26       AGAACATTAT CTTACCTTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
27       AAATAATCAG GAAGTGTGTT TCCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
28       CCCTAACGAC CAACTTGCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
29       GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
30       GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
31       GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
32                                   (start HD-73)                   CCT ATGTTCTCTT
33       GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
34       ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
35       TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
36       GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
37       TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
38       GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
39       TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
40       TATTTTGAAG GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
41       TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
42       TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

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30 CAGAAGGCGG TGAATGCGCT GTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 31 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
 32 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGAAATA 2500
 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 33 ACACTATCAG GTACCTTTGA TGAATGCTAT CCAACATATT TGTATCAAAA 2600
 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAGAGGGGT
 34 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
 35 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC
 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGCCAC 2800
 36 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 37 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTCATG TAGGATGTAC 2900
 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 38 AAGATGGGCA CGCAAGACTA GGAATCTAG AGTTTCTCGA AGAGAAACCA 3000
 39 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 AGACAAACGT GAAAAATTGG AATGGGAAAC AATATCGTT TATAAGAGG 3100
 40 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 41 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 TAGCATTCTGA GAAGCTTATC TGCTGAGCT GTCTGTGATT CCGGGTGTCA
 42 ATGCGGCTAT TTTTGAAGAA TTAGAAGGCG GTATTTTCAC TGCATTCTCC 3300
 43 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 44 AACGTTGCGT CTTGTGTTT CCGGAATGGG AAGCAGAAAT GTCACAAGAA
 45 GTTCGTGTCT GTCCGGGTCG TGGGTATATC CTTCTGTCA CAGCGTACAA 3500
 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 46 CAGACGAACT GAAGTTTAGC AATGCGTAG AAGAGGAAAT CTATCCAAT 3600
 47 AACACGGTAA CGTGTAAATG TTATACTGTA AATCAAGAAG AATACGGAGG
 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 48 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 49 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 50 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
 51 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
 T G Y T F I D I S L S L T Q F L L S E F V P G A G F V L G L
 55 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
 56 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 57 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 58 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 59 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 60 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 61 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T

62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
 63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
 64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
 65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
 66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
 67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
 68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
 69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
 70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
 71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
 72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
 73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
 74 Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R
 75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
 76 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
 77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
 78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
 79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
 80 I V Y K E A K E S V D A L E V N S Q Y D Q L Q A D T N I A M
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
 E I E N N T D E L K F S N C Y E E E I Y P N N T V T C N D Y
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
 S V E L L L M E E .

23. A pesticidal composition, according to claim
 12, wherein said gene, denoted pACB-1, encoding a
 chimeric toxin, is as follows:

(start HD-73) ATG GATAACAATC 400
 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 TTCTTGTCTG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC

16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 20 ATCCAATTCT AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 21 GATTAGAAA ATTTTGATGG TAGTTTTGCA GGCTCGGCTC AGGGCATAGA
 22 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 23 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAATA
 24 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCTT TTCGCTATA 1400
 25 TGGAACATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 26 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 29 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 30 CCTAGGCAAG AATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700
 31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 32 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 33 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 35 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 37 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 38 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 40 CTTTTCAAAT GGATCAAGTG TATTAGGTT AAGTGCTCAT GTCTTCAATT 2300
 41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAGTA
 42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAGAG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 45 TGCTGGATG AAAAACAGAG ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAG AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 52 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 56 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 59 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 63 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 64 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT

66 CTTCCGGAAT GGGGAAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 68 GTTGCCTAAC CATTATGAG ATCAGAGACA ATACAGACGA ACTGAAGTTT 3700
 69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 ACB-1 with the following amino acid sequence:

79 MDNNPNINECIPYNCLSNFEVEVLGGERIE
 80 TGYTPIDISLSLTQFLLEFVPGAGFVLGL
 81 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
 82 FARNQAIISRLEGLSNLYQIYAESFREWEAD
 83 PTNPALREEMRIQFNDMNSALTTAIPLFAV
 84 QNYQVPLLSVYVQAANLHLSVLRDVSFVGQ
 85 RWGFDAATINSRYNDLTRLIGNYTDYAVRW
 86 YNTGVALERVWGPDSRDWVRYNQFRRELTLT
 87 LDIVALELFPNYDSRRYPVRTVSQLTREIYTN
 88 PVLENFDFGSGFRGSAQGIERSIRSPHLMIDL
 89 NSITIIYTDHARGYYYSWGHQIMASPVGFSG
 90 PEFTTFPLYGTMGNAAPQQRIVAQLGQGVYR
 91 TLSSTLYRRPFNIGINNQQLSVLDGTEFAY
 92 GTSSSNLPSAVYRKSGTVDSLNEIPPQNNNV
 93 PPRQEFSHRLSHVSMFRSGFSNSSSVSIIRA
 94 PTFSSWQHRSAEFNNIIPSSQITQIPLTGST
 95 NLGSGTSTSVVKGPFGFTGGDILRRTSPGGQIST
 96 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
 97 IDGRFINQGNFSATMSSGGSNLQSGGSFRTVG
 98 FTTFFNFNSNGSSSVFTLSAHVFNSGNEVYID
 99 RIEFVFAEVTFEAEYDLERAQKAVNELFTS
 100 SNQIGLKTDTVTDYHIDQVSNLVECLSD EFC
 101 LDEKRELSEKVKHAKRLSDERNLLQDPNFR
 102 GINRQLDRGWRGSTDITIQGGDDVFKENYV
 103 TLLGTTFDECYPTYLYQKIDESKLLKAYTRYQ
 104 LRGYIEDSQDLEIYLI RYN AKHETVNVPGT
 105 GSLWFLSAQSPIIGKCGEPNRCAPHLEWNPD
 106 LDCSCRDGEKCAHHSHHFSLDIDVGC TDLN
 107 EDLGVWVIFKIKTDG HARLGNLEFLEEK P
 108 LVGEALARVKRAEKKWRDKREKLEWETNIV
 109 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 110 AADKRVHSIREAYLPELSVIPGVNA AIFEE

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111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S Q W
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 118 E L L L M E E .

1 24. A pesticidal composition, according to
 2 claim 12, wherein said gene, denoted pSYW1, encoding
 3 a chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400
 5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 6 GAAGTATTAG GTGGAGAAAG AATAGAAACT GTTACACCC CAATCGATAT 500
 7 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCGGTGCTG
 8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 9 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 10 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
 11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 12 ACTAATCCAG CATTAGAGA AGAGATSCGT ATTCAATTCA ATGACATGAA 800
 13 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
 14 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 15 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 20 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 21 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA
 22 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 23 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
 24 ATGGCTTCTC CTGTAGGGTT TTGGGGGCCA GAATTCACCT TTCCGCTATA 1400
 25 TGGAACTATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 26 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 29 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 30 CCTAGGCAAG GATTTAGTCA TCGATTAGC CATGTTTCAA TGTTCGTTT 1700
 31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 32 (start HD-1) CCAACGT TTTCTTGGA GCATCGCAGT 1900
 33 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTACCTGG CCAGATTTCA
 36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 37 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 38 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 40 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA

42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTTCATC AGATGAATTT 2500
 45 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 47 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 50 TAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAGCAGTAAA
 52 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGSATG TACAGACTTA AATGAGGACC
 56 TAGGTGATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAATAAT 3200
 59 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGCG TCAATGCGGC TATTTTGTGA 3400
 63 GAATTAGAAG GCGGTATTTT CACTGCTATC TCCCTATATG ATGCGAGAAA
 64 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTG
 66 CTTCCGGAAT GGGAGGAGAA AGGTGCAAAA GAAGTTCGTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 68 GTTGCCTAAC CATTATGAG ATCGAGAAAT ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATAAGG AGGTGCGTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 72 TATGAAGAAA AATCGTATAC AGATGACGGA AGAGAGAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAGGGATT ACAGGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCA GAACCGSATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 SYW1 with the following amino acid sequence:

79 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 88 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
 89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
 90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 92 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V
 93 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D F E F C
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 102 G I N R Q L D R G W R G S T D I T I Q G G D V F K E N Y V
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 105 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 113 V R V C P G R G Y I L R Y T A Y K E G Y G E G C V T I H E I
 114 E N N T D E L K F S N C V E E I Y P N N T V T C N D Y T V
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 118 E L L L M E E

1 25. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid sequence:

5 (start HD-73) ATG GATAACAATC 400
 6 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 7 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 8 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 9 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 10 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 11 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 12 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 13 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800
 14 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 15 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 16 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 17 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AAETATACAG 1000
 18 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 19 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 20 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 21 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 22 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA

23 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 24 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
 26 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 27 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 30 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 31 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700
 32 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 33 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900
 34 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 35 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 36 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGCG CCAGATTTCA
 37 ACCTTAAGAG TAAATATTAC TGCACCATTG TCACAAAGAT ATCGGGTAAG 2100
 38 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 39 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 41 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 43 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAGG CGGTGAATGA 2400
 44 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATTT 2500
 46 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAGTCAAAC ATGCGGATCA 2600
 47 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA
 48 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 49 GGAGGCGATG ACGTATTCAA AGAGATTAC GTTACGCTAT TGGGTACCTT 2700
 50 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 51 TAAAGCCTA TACCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 52 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 53 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 54 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 55 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 56 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 57 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 58 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 59 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 60 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 61 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 62 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 63 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGTAA 3400
 64 GAATTAGAAAG GGCATTTTT CACTGCATTG TCCCTATATG ATGCGAGAAA
 65 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTG
 67 CTTCCGGAAT GGGGAGCAGA AGTGTCACAA GAAGTTCGTG TCTGTCCGGG 3600
 68 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 69 GTTGGGTAA CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 72 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 74 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 75 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 76 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 77 GGAA (end HD-1).

26. A recombinant DNA transfer vector comprising
DNA having the following nucleotide sequence or
equivalent nucleotide sequences containing bases whose
translated region codes for the same amino acid sequence:

(start HD-1) ATGG ATAACAATCC GAACATCAAT

GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
ATTTCTTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCG 800
CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
CGCTGGTACA ATACGGGATT AGAGCTGTGA TGGGGACCGG ATTCTAGAGA 1200
TTGGGTAAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
ACAGTTTCCC AATTAACAAG AGAATTTAT ACGAACCCAG TATTAGAAAA
TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAATAAA CAGCTTCTCC 1500
TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGAAATGCGG
GGAATGCAGC TCCACCCGTA GTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
AGAACATTAT CTTACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTTGCC 1700
CCCTAACGAC CAACTTGCTT TCCACTATAT ATAGACAAAG GGGTACAGTC
GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)

(start HD-73) CCT ATGTTCTCTT

GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
TTCAGSACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
GATTACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGSTA ATATTAGAGG
TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC ATATTGTAAT 2200
TTATTCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
AACAATGTG ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
AAATTTCAA GACATTAATA GGCAACCAGA ACGTGGGTGG GCGGGAAGTA 2500
CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGA AAATTACGTC
ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT

52 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCTG CTACAATGCA 2700
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC
 54 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 56 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 57 AAGATGGGCA CGCAAGACTA GGAATCTAG AGTTTCTCGA AGAGAAACCA 3000
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 60 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 61 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 62 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 63 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTTCAC TGCATTCTCC 3300
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTCTA ATAATGGCTT
 66 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 67 AACGTTGCGT CCTTGTGTGT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 68 GTTCGTGTCT GTCCGGGTCT TGGCTATATC CTTGTGTCTA CAGCGTACAA 3500
 69 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 70 CAGACGAAC TGAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 71 AACACGGTAA CGTGAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 72 TGCGTADACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 73 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 74 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 75 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATATCGT GGACAGCGTG 3900
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 12 AGAAGAAATC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 13 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 16 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTAGTGTG TGGACAAAGG TGGGGATTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT

22	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
23	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
24	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
25	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
26	ATGGCTTCTC	CTGTAGGGTT	TTCGGGGCCA	GAATTCACCT	TTCCGCTATA	1400
27	TGGAACATATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
28	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACDTTTT	1500
29	AATATAGGGA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	
30	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
31	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
32	CCTAGGCAAG	AATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTC	1700
33	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
34	(start	HD-1)	CCAACGT	TTTCTTGCCA	GCATCGCAGT	1900
35	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
36	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCTGT	AAAGGACCAG	2000
37	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
38	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
39	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
40	GAAGACCTAT	TAATCAGGGT	AATTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
41	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCGGTTTAA	
42	CTTTTCAAAT	GGATCAAGTG	TATTTAGGTT	AAGTGCTCAT	GTCTTCAATT	2300
43	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAASTA	
44	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
45	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
46	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
47	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
48	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
49	ATAGACAAC	AGACCTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
50	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
51	TGATGAGTGC	TATCGAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
52	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
53	GACTTAGAAA	TGTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
54	TGTGCCAGGT	ACGGGTTTCT	TATGSCCGCT	TTCAGCCCAA	AGTCCAATCG	2900
55	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
56	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTGCGA	3000
57	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
58	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
59	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAGAGCGT	
60	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
61	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
62	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
63	TGCCATGATT	CATGCGGCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
64	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
65	GAATTAGAAG	GGCGTATTTT	CACTGCATTG	TCCCTATATG	ATGCGAGAAA	
66	TGTCATTAAG	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
67	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTC	GGTCTTGTG	
68	CTTCCGGAAT	GGGAAGCAGA	AGTGTCACAA	GAAGTTCTGT	TCTGTCCGGG	3600
69	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	
70	GTTGCGTAAC	CATTCATGAG	ATCGAGAACA	ATACAGACGA	ACTGAAGTTT	3700
71	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	

72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 28. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATATT GTTTAAGTAA CCTGGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTGT ACAATTGAA CAGTTAATTA ACCAAGAAT
 12 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 13 ATCTTTATCA AATTTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
 16 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 22 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 23 GTATTAGAAA ATTTTGATGG TAGTTTTGGA GGCTCGGCTC AGGGCATAGA
 24 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 25 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 27 TGGAACATAG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 28 GTCAGGGCGT GTATAGAACCA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 31 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 32 CCTAGGCAAG GATTTAGTCA TCGATTAGC CATGTTTCAA TGTTCGTTT 1700
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 34 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 35 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 36 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 37 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 38 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 39 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG

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40 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 42 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGSAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 47 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 49 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAGGCGATG ACGTATTCAG AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 54 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCGAA AGTCCAATCG 2900
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGSAATC TAGAGTTTCT CGAAGAGAAA CATTAGTAGG GAGAAGCGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 61 TGGAAATGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 63 TGCCATGATT CATGCGGCGG ATAGACGTTT TCATAGCATT CGAGAAGCTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 65 GAATTAGAAAG GGCSTATTTT CACTGCAATC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTCAACA GAAGTTCGTG TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTTCGTG TGACAGCGTA CAAGGAGGGA TATGAGAAAG
 70 GTTGCGTAAC CATTATGAG ATCGAACAACA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGGTCAATC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-
 2 ferred to and replicated in a prokaryotic or lower
 3 eukaryotic microorganism.

1 30. The DNA transfer vector of claim 26 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 31. The DNA transfer vector of claim 27 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 32. The DNA transfer vector of claim 28 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 33. Plasmid pEW1 as shown in FIGURE 1 of the
2 drawings.

1 34. Plasmid pEW2 as shown in FIGURE 2 of the
2 drawings.

1 35. Plasmid pEW3 as shown in FIGURE 3 of the
2 drawings.

1 36. Plasmid pEW4 as shown in FIGURE 4 of the
2 drawings.

1 37. Plasmid pACB-1, having the construction of
2 plasmid pEW3 except that the DNA encoding aspartic
3 acid at position 411 is converted to encode asparagine,
4 and the DNA encoding glycine at position 425 is con-
5 verted to encode glutamic acid.

1 38. Plasmid pSYW1, having the construction of plasmid
2 pEW3 except that the DNA encoding arginine at position
3 289 is converted to encode glycine, the DNA encoding
4 arginine at position 311 is converted to encode lysine,
5 and the DNA encoding tyrosine at position 313 is conver-
6 ted to encode glutamate.

1 39. A microorganism transformed by the transfer
2 vector of claim 25.

1 40. A microorganism transformed by the transfer
2 vector of claim 26.

1 41. A microorganism transformed by the transfer
2 vector of claim 27.

1 42. A microorganism transformed by the transfer
2 vector of claim 28.

1 43. E. coli (pEW3), a microorganism according
2 to claim 39.

1 44. E. coli (pEW4), a microorganism according to
2 claim 40.

1 45. E. coli (pACB-1), a microorganism according
2 to claim 41.

1 46. E. coli (pSYW1), a microorganism according
2 to claim 42.

1 47. A process for preparing pesticidal chimeric
2 toxin EW3 having the following amino acid sequence:

3 MDNNFNI NE C I F Y N C L S N F E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G F S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N F A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W S F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 F V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y W S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
 17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 18 P T F S W Q H R S A E F N N I I F S S Q I T Q I F L T K S T
 19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 20 L R V N I T A F L S Q R Y R V R I R Y A S T T N L Q F H T S
 21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 27 T L L G T F D E C Y F T Y L Y Q K I D E S K L K A Y T R Y Q
 28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V F G T
 29 G S L W F L S A Q S F I G K C G E F N F C A P H L E W N P D
 30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 31 E D L G V W V I F K I K T Q D G H A F L G N L E F L E E K P
 32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 36 N V K G H V D V E E Q N N R S V L V L P E W E A E V S Q E
 37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 39 N Q E E Y G G A Y T S R N E G Y N E A P S V P A D Y A S V Y
 40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pEW3, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
 50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 51 GAAATATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 52 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 54 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 55 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 56 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 58 CAGTGGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 59 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 60 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC

61	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG	1000
62	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAAGCTGT	ATGGGGACCG	
63	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
64	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
65	ATCCAATTCT	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
66	GTATTAGAAA	ATTTTGATGG	TAGTTTTTCA	GGCTCGGCTC	AGGGCATAGA	
67	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
68	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAATA	
69	ATGGCTTCTC	CTGTAGGGTT	TTGCGGGCCA	GAATTCACCT	TTCCGCTATA	1400
70	TGGAAGTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
71	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
72	AATATAGGGA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	
73	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
74	GAACGGTAGA	TTCGCTGGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
75	CCTAGGCAAG	GATTTAGTCA	TGATTAAGC	CATGTTTCAA	TGTTTCGTTT	1700
76	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
77	(start	HD-1)	CCAACGT	TTTCTTGGA	GCATCGCAGT	1900
78	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATACAC	AAATACCTTT	
79	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCGTT	AAAGGACCAG	2000
80	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTACCTGG	CCAGATTTCA	
81	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
82	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
83	GAAGACCTAT	TAATCAGGGT	AATTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
84	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
85	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTCTCAT	GTCTTCAATT	2300
86	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
87	ACCTTTGAGG	CAGAATATGA	TTTAGAAGA	GCACAAAAGG	CGGTGAATGA	2400
88	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
89	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTCATC	AGATGAATTT	2500
90	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
91	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
92	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
93	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
94	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAT	
95	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
96	GACTTAGAAA	TCTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
97	TGTGCCAGGT	ACGGGTTTCT	TATGCCCGCT	TTACGCCCAA	AGTCCAATCG	2900
98	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
99	GACTTAGATT	GTTGCTGTAG	GGATGGAGAA	AAGTGTGCC	ATCATTCGCA	3000
100	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
101	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
102	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAGCGCT	
103	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
104	TGGAATGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
105	GCTTTATTGG	TAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
106	TGCCATGATT	CATGCGGCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
107	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTGA	3400
108	GAATTAGAAG	GGCGTATTTT	CACTGCATTC	TCCCTATATG	ATGCGAGAAA	
109	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
110	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCTTGT	
111	CTTCCGGAAT	GGGAAGCAGA	AGTGTACAAA	GAAGTTCTGT	TCTGTCCGGG	3600
112	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	
113	GTTGCGTAAC	CATTCATGAG	ATCGAGAACA	ATACAGACGA	ACTGAAGTTT	3700
114	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
120 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric
2 toxin EW4 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
14 P E F A F P L F G N A G N A A F P V L V S L T G L G I F R T
15 L S S P L Y R R I I L G S G F N N Q E L F V L D G T E F S F
16 A S L T T N L P S T I Y R R G T V D S L D V I P P Q D N S
17 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
19 N F L F N G S V I S G F G F T G G D L V R L N S S G N N I Q
20 N R G Y I E V F I H F P S T S T R Y R V R V R Y A S V T P I
21 H L N V N W G N S S I F S N T V F A T A T S L D N L Q S S D
22 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
24 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
26 F K D I N R Q F E R G W G G S T G I T I Q G G D D V F K E N
27 Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
29 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
42 S V E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pEW4, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same amino
 48 acid sequence:

49 (start HD-1) ATGG ATAACAATCG GAACATCAAT
 50 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
 51 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCG
 52 TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
 53 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCTCTCTC AATGGGACGC
 54 ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAGAATA GAAGAATTG 800
 55 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
 56 ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
 57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
 58 CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
 59 TCAGTATATG TTCAAGCTGC AATTTACAT TTATCAGTTT TGAGAGATGT
 60 TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
 61 GTTATAATGA TTTAACTAGG CTTATGGCA ACTATACAGA TTATGCTGTG
 62 CGCTGGTACA ATACGGGAT AGAGCTGTGA TGGGGACCGG ATTCTAGAGA 1200
 63 TTGGGTAAAG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
 64 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
 65 ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
 66 TTTTGATGGT AGTTTTCGTG GAATGCTCA GAGAATAGAA CAGAATATTA 1400
 67 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
 68 GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
 69 TGTAGGGTTT TCAGGACGAG AATTCGCATT CCCTTTATTT GGGAATGCGG
 70 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
 71 AGAACATTAT CTTACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
 72 AAATAATCAG GAAGTGTTC TCCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
 73 CCCTAACGAC CAAGTTGCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
 74 GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGATC CACCTCGTGC 1800
 75 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
 76 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
 77 (start HD-73) CCT ATGTTCTCTT
 78 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
 79 ACTCAAATCC CTGCAGTGAA GGGAACTTT CTTTTAATG GTTCTGTAAT
 80 TTCAGGACCA GGATTTACTG GTGGGACTT AGTTAGATTA AATAGTAGTG 1900
 81 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCAGTCCCA
 82 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
 83 GATTCACCTC AACGTTAATT GGGGTAATC ATCCATTTTT TCCAATACAG
 84 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
 85 TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
 86 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
 87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

88 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
 89 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 90 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 91 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
 92 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GCGGGAAGTA 2500
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 94 ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
 95 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
 96 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GCGCGCTTTC
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 100 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 102 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 105 CAAAAGAATC TGATAGTGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 106 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 107 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 108 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 109 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 111 AACGTTGCGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 112 GTTCGTGTCT GTCCGGGTCTG TGGGTATATC CTTGCTGTCA CAGCGTACAA 3500
 113 GGAGGGGATAT GGAGAAGGTT GCCTAACCAT TCATGAGATC GAGAACAATA
 114 CAGACGAACG GAAGTTTAGC AACTGGGTAG AAGAGGAAAT CTATCCAAT 3600
 115 AACACGGTAA CGTGTAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 116 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 117 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 118 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 119 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 120 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 121 GAATTACTCC TTATGGAGGA A (end HD-73).

49. A process for preparing pesticidal chimeric
 toxin ACB-1 having the following amino acid sequence:

3 M D N N P N I N E C I F Y N C L S N F E V E V L G G E R I E
 4 T G Y T F I D I S L S L T Q F L L S E F V F G A G F V L G L
 5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 7 P T N F A L R E E M R I Q F N D M N S A L T T A I F L F A V
 8 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 9 R W S F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 10 Y N T G L E R V W G F D S R D W V R Y N Q F R R E L T L T V
 11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 16 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 17 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 23 R I E F V P A E V T F E A E Y D L E R A Q K A Y N E L F T S
 24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 29 G S L W P L S A Q S P I G K C G E F N E C A P H L E W N P D
 30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pACB-1, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49	(start HD-73)	ATG GATAACAATC	400
50	CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA		
51	GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT	500	
52	TTCTTGTGCT CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGTCTG		
53	GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT	600	
54	CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT		
55	AGAGAAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGAATAAGCA	700	
56	ATCTTTATCA AATTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT		
57	ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA	800	
58	CAGTGGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG		
59	TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT	900	
60	TTGAGAGATG TTTCAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC		

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTCTG AACAGTTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
66 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAATA
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCTT TTCCCTATA 1400
70 TGSAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG AATTTAGTCA TCGATTAAAG CATGTTTCAA TGTTTCGTT 1700
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATACAC AAATACCTTT
79 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
80 GATTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
81 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
83 GAABACCTAT TAATCAGGGT AATTTTTGAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
85 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
90 TGCTGSGATG AAAACAAGA ATTTGTCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
92 ATAGACAACCT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
93 GGAGGCGATG ACGTATTCAG AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
95 TAAAAGCCTA TACCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAA
97 TGTGCCAGGT ACGGTTTCTT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
98 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
102 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
103 AGCTCGTGAG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
104 TGSAATGGA AACAAATATC GTTTATAAG AGGCAAAAGA ATCTGTAGAT
105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
106 TGCCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
107 ATCTGCCTGA GCTGTCTGTG ATTCGGGGTG TCAATGCGGC TATTTTTGAA 3400
108 GAATTAGAAG GCGGTATTTT CACTGCATTG TCCCTATATG ATGCGAGAAA
109 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTTGTT
111 CTTCCGGAAT GGGAAAGCAGA AGTGTCAACA GAAGTTCGTG TCTGTCCGGG 3600
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG

113 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 121 GGAA (end HD-1) .

1 50. A process for preparing pesticidal chimeric
 2 toxin SYW1 having the following amino acid sequence:

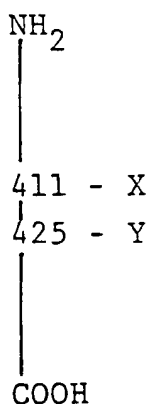
3 MDNNPNINECIPYNCLSNPEVEVLGGGERIE
 4 TGYTPIDISLSLTQFLLEFVFGAGFVVLGL
 5 VDIIWGIFGFSQWDAFLVQIEQLINQRIEE
 6 FARNQAIISRLEGLSNLYQIYAESFREWEAD
 7 PTNPALREEMRIQENIMNSALTTAIFLFAV
 8 QNYQVPLLSVYVQAAMHLHSVLRDVSVFGQ
 9 RWGFDAAATINSRYNDLTRLIGNYTDYAVRW
 10 YNTGLERVWGPDSRWVRYNQFRRELTLTV
 11 LDIVALLFPNYDSRYFIRTVSGLTREIYTN
 12 PVLENFDGSGFRGSAQGIEGSIIRSPHLMIL
 13 NSITITYTDAAHKGLEYYSGHQIMASPVGFSG
 14 PEFTTFPLYGTMBNAPQQRIVAQLGGGVYR
 15 TLSSTLYRRPBNIGINNQQLSVLDGTEFAY
 16 GTSSSNLPSAVYRKSGTVDSLDEIPPQNNNV
 17 PPRQGGSFHRLSHVSMFRSGFSNSVSIIRA
 18 PTFSWQHRSAEFNNIIFSSQITQIPLTKST
 19 NLGSGGTSVVKGPFGFTGGDILRRTSPGQIST
 20 LRVNITAFLSQRYRVRIRYASTTNLQFHTS
 21 IDGRPINQGNFSATMSSSGSNLQSGGSFRTVG
 22 FTTFPNFNSNGSSSVFTLSAHVFNSGNEVYID
 23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 24 SNQIBLKTDTVTDYHIDQVSNLVECLSDFC
 25 LDEKQELSEKVKHAKRLSDERNLLQDFNFR
 26 GINRQLDRGWGSGTDITIQGGDDVFKENYV
 27 TLLGTFFDECYPTYLYQKIDESKLYTRYQ
 28 LRGYIEDSQDLEIYLIRYNKHETVNVPGT
 29 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP
 30 LDCSCRDGEEKCAHHSHHFSLDIDVGGCTDLN
 31 EDLGVWVIFKIKTQDGHARLGNLEFLEEK
 32 LVGEALARVKRAEKKWRDKREKLEWETNIV
 33 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 34 AADKRVHSIREAYLPELSVIPGVNAAFIEE
 35 LEGRIFTAFSLYDARNVIKNGDFNNGLSQW
 36 NVKGHVDEEENNRQSVLVLPWEAEVSEI
 37 VRVCPGRGYILRVTAKEGYGEGCVTIHEI
 38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
 39 NQEEYGGAYTSRNRGYNEAFSPADYASVY
 40 EEKSYTDGRRENPCFNRGYRDYTFPLRVGY
 41 VTKELEYFPETDKVWIEIGETEGTFIVDSV
 42 ELLLMEE

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pSYW1, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
 50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCTGAAGTA
 51 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
 52 TTCTTGTCG CTAACGCAAT TTCTTTGAG TGAATTTGT CCCGGTGCTG
 53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTT TGGTCCCTCT 600
 54 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 55 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
 56 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 57 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 58 CAGTGCCTTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
 59 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 60 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 61 TATCAATAGT CGTTATAATG ATTTACTAG GCTTATGSC AACTATACAG 1000
 62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAGAG AATTAACACT 1100
 64 AACTGTATTA GATATCGTTG CTCTGTSCC GAATTATGAT AGTAGAAGAT
 65 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 66 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
 67 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 68 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAATA
 69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
 70 TGGAACTATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 71 GTCAGGGCGT GTATAGAACTA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 73 TGCTTATGGA ACCTCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 74 GAACGGTAGA TTCTCTGAT GAAATACGCG CACAGAATAA CAACGTGCCA
 75 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTT 1700
 76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 77 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCTT AAAGGACCAG 2000
 80 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 81 ACCTTAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 82 AATTGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 83 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACATAGAG TAGTGGGAGT 2200
 84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 85 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 86 GAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 88 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 90 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 92 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA

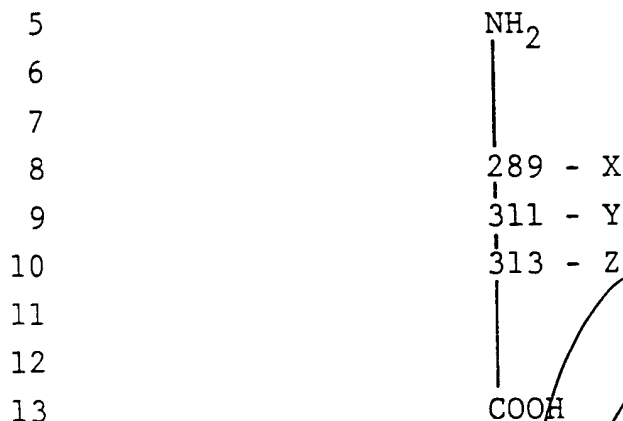
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 95 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 97 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 98 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 99 GACTTAGATT GTTCGTGTAG GGTAGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 102 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 103 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 104 TGGTAATGGG AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 106 TGCCATGATT CATGCGGCGA ATAAACGTGT TCATAGCATT CGAGAAGCTT
 107 ATCTGCCTGA GCTGTCTGTG ATTCGCGGTG TCAATGCGGC TATTTTTGAA 3400
 108 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 109 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 110 AAGGSCATGT AGATGTAGAA GAACAAAACA ACCACGTTT GGTCTTGTG
 111 CTTCCGGAAT GGGAGCGAGA AGTGTACAGA GAGTTCTGTG TCTGTCCGGG 3600
 112 TCGTGGCTAT ATCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 113 GTTGCCTAAC CATTCATGAG ATCGAGACCA ATACAGACGA ACTGAAGTTT 3700
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 117 TATGAAGAAA AATCGTATAC AGATGATCGA AGAGAGAATC CTTGTGAATT 3900
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 121 GGAA (end HD-1).

51. A chimeric toxin, having the amino acid sequence of toxin EW3, with changes which can be shown schematically as follows:



13 wherein X is one of the 20 common amino acids
14 except Asp when the amino acid at position 425 is
15 Gly; Y is one of the 20 common amino acids except
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



15 wherein X is one of the 20 common amino acids except
16 Arg when the amino acid at position 311 is Arg and the
17 amino acid at position 313 is Tyr; Y is one of the 20
18 common amino acids except Arg when the amino acid at
19 position 289 is Arg and the amino acid at position 313
20 is Tyr; and Z is one of the 20 common amino acids
21 except Tyr when the amino acid at position 289 is
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in
2 claim 51.

1 54. DNA encoding a chimeric toxin as shown in
2 claim 52.

1 55. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 51.

1 56. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 52.

1 57. A chimeric toxin comprising the variable
2 region or regions of two or more Bacillus toxins.

1 58. A toxin, according to claim 57, wherein the
2 Bacillus toxins are B. thuringiensis toxins.

1 59. A toxin, according to claim 58, wherein the
2 B. thuringiensis toxins are B. thuringiensis var.
3 kurstaki HD-1 toxin and B. thuringiensis var. kurstaki
4 HD-73 toxin.

1 60. A toxin, according to claim 58, wherein
2 the B. thuringiensis toxins are encoded by a pesticide-
3 producing strain of Bacillus thuringiensis, consisting
4 of B. thuringiensis M-7, B. thuringiensis var. kurstaki,
5 B. thuringiensis var. finitimus, B. thuringiensis var.
6 alesti, B. thuringiensis var. sotto, B. thuringiensis
7 var. dendrolimus, B. thuringiensis var. kenyae, B.
8 thuringiensis var. galleriae, B. thuringiensis var.
9 canadensis, B. thuringiensis var. entomocidus, B.
10 thuringiensis var. subtoxicus, B. thuringiensis var.
11 aizawai, B. thuringiensis var. morrisoni, B. thuringiensis
12 var. ostrinae, B. thuringiensis var. tolworthi, B.
13 thuringiensis var. darmstadiensis, B. thuringiensis
14 var. toumanoffi, B. thuringiensis var. kyushuensis, B.
15 thuringiensis var. thompsoni, B. thuringiensis var.
16 pakistani, B. thuringiensis var. israelensis, B. thurin-
17 giensis var. indiana, B. thuringiensis var. dakota,

18 B. thuringiensis var. tohokuensis, B. thuringiensis
19 var. kumanotoensis, B. thuringiensis var. tochigiensis,
20 B. thuringiensis var. colmeri, B. thuringiensis var.
21 wuhanensis, B. thuringiensis var. tenebrionis, B.
22 thuringiensis var. thuringiensis, and other Bacillus
23 species selected from B. cereus, B. moritai, B.
24 popilliae, B. lentimorbus, and B. sphaericus.

add
Q5

2025-06-06 14:00:00